

Supplementary Figures

Figure S1. Organization of Mexico into three regions, north (blue), central (pink), and south (green) for viral migration analysis. To better characterize the viral diffusion in the region, Mexico was divided into 3 main regions: (1) the Northern Region (states of Baja California, Jalisco, Tamaulipas, Nuevo Leon, Sonora, Sinaloa, Colima, Chihuahua), (2) the Central Region (states of Puebla, Distrito Federal, Estado De Mexico, Morelos, Oaxaca, Michoacan, Guerrero, Tlaxcala, Hidalgo) and (3) the Southern region (states of Quintana Roo, Yucatan, Veracruz, Campeche, Tabasco, Chiapas).

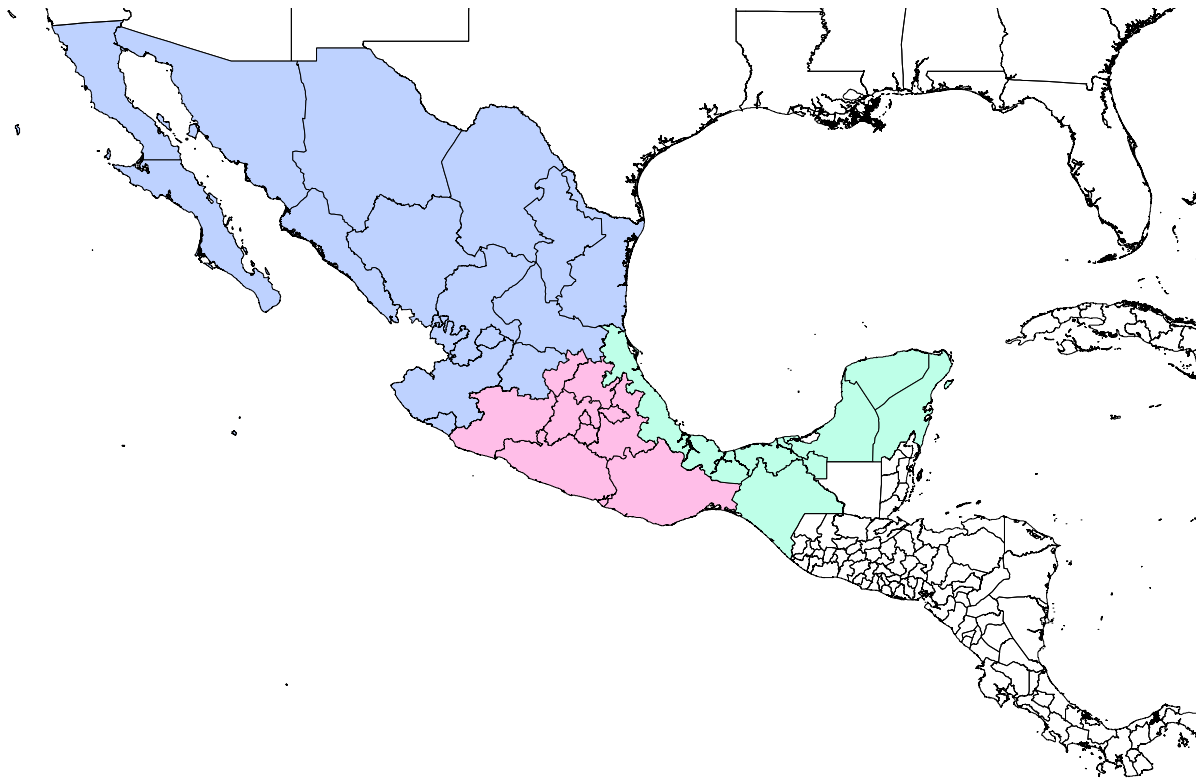


Figure S2. Time to most recent common ancestor estimation for the large transmission clusters. Phylogenetic reconstruction and estimation of the time to most recent common ancestor (TMRCA, years) of the largest clusters ($n > 10$) was performed using a Markov Chain Monte Carlo framework as implemented in BEAST v1.8.1 (1) with BEAGLE to improve run-time (2). We used a discretized gamma distribution (GTR + 4 Γ) to account for among-site rate variation. Time scales of the trees were calibrated with the sampling dates available. Tips are colored by the county of origin for Guatemala and Mexico Clusters.

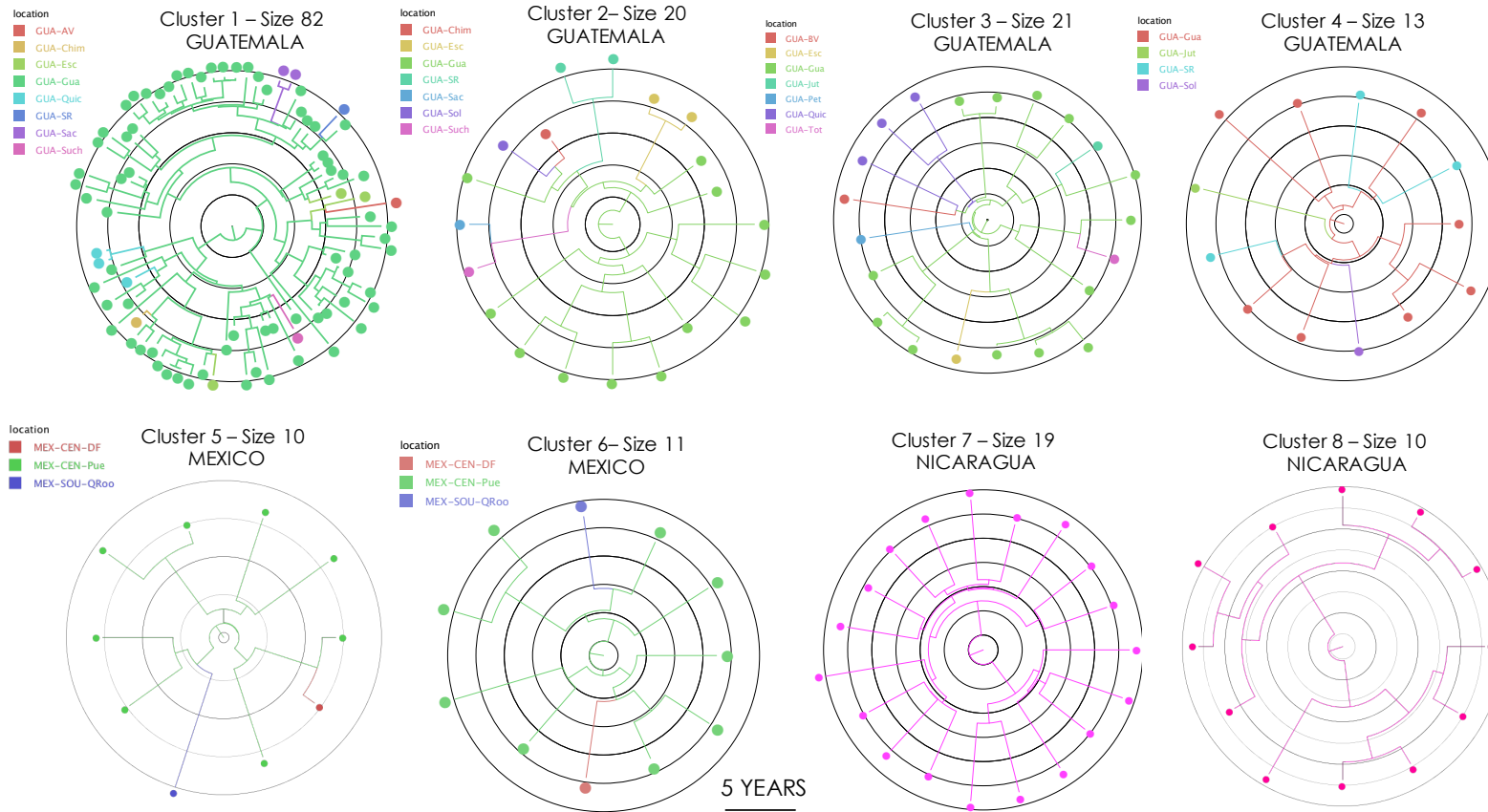


Figure S3. Viral gene flow of the sampled Mesoamerican epidemic between nations. Distribution of migration events for each of 100 subsamples. Viral migration was inferred using the Slatkin-Maddison index on phylogenetic trees constructed from 100 random subsets of equal number of sequences per location pair. Red asterisks indicate viral migration routes (source to destination) that were significantly higher than expected.

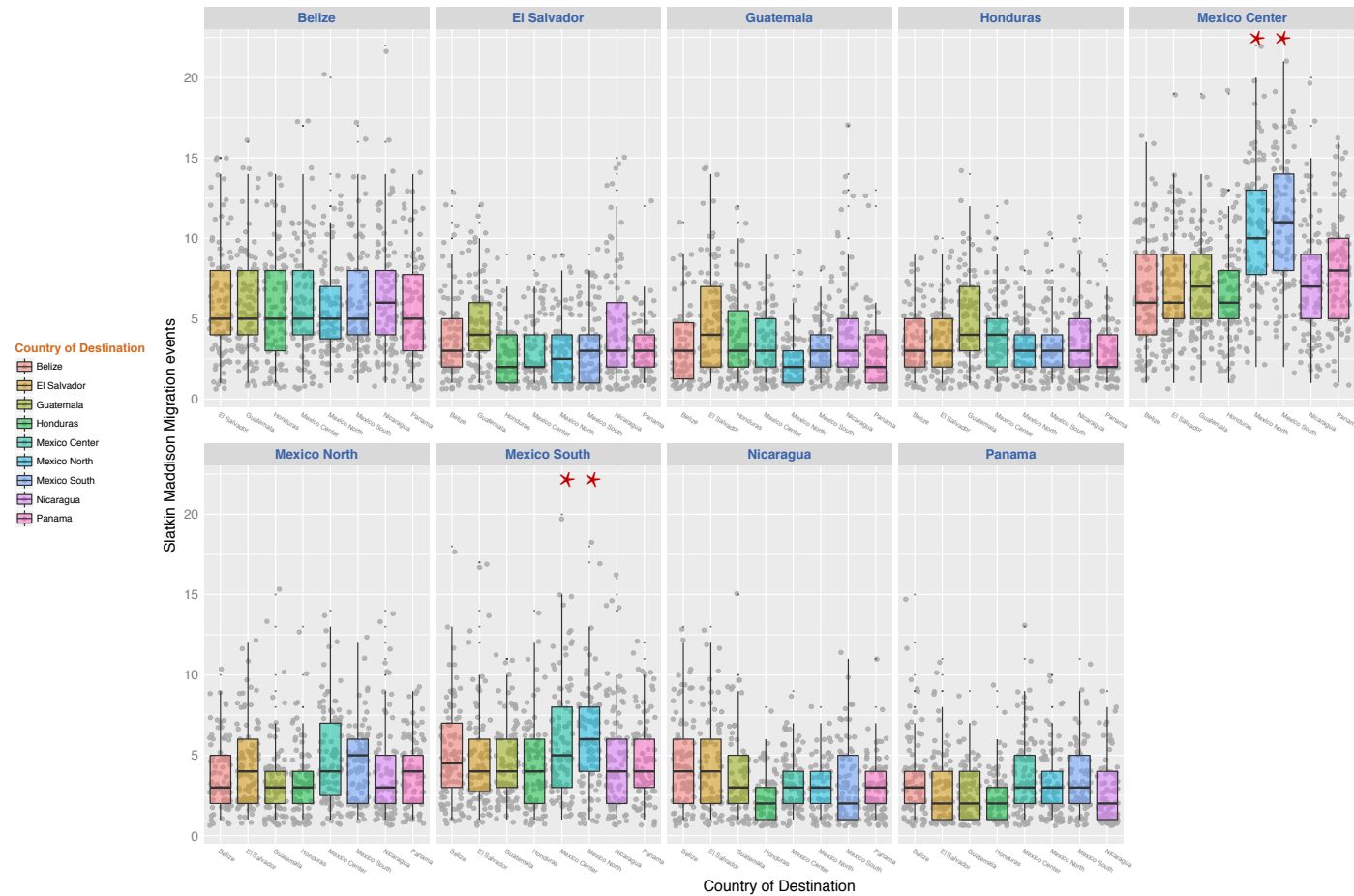


Figure S4. Viral gene flow between the sampled Mesoamerican epidemic and the United States. Viral migration was inferred using the Slatkin-Maddison index on phylogenetic trees constructed from 100 random subsets of equal number of sequences per location pair. HIV-1 subtype B sequences collected during the same time period in the US were downloaded from the Los Alamos National Laboratory (LANL) HIV sequence database on May 23th 2017. Red asterisks indicate viral migration routes (source to destination) that were significantly higher than expected. **3A.** Migration Events from the US toward the Mesoamerican locations. **3B.** Migration Events from Mesoamerican locations toward the US.

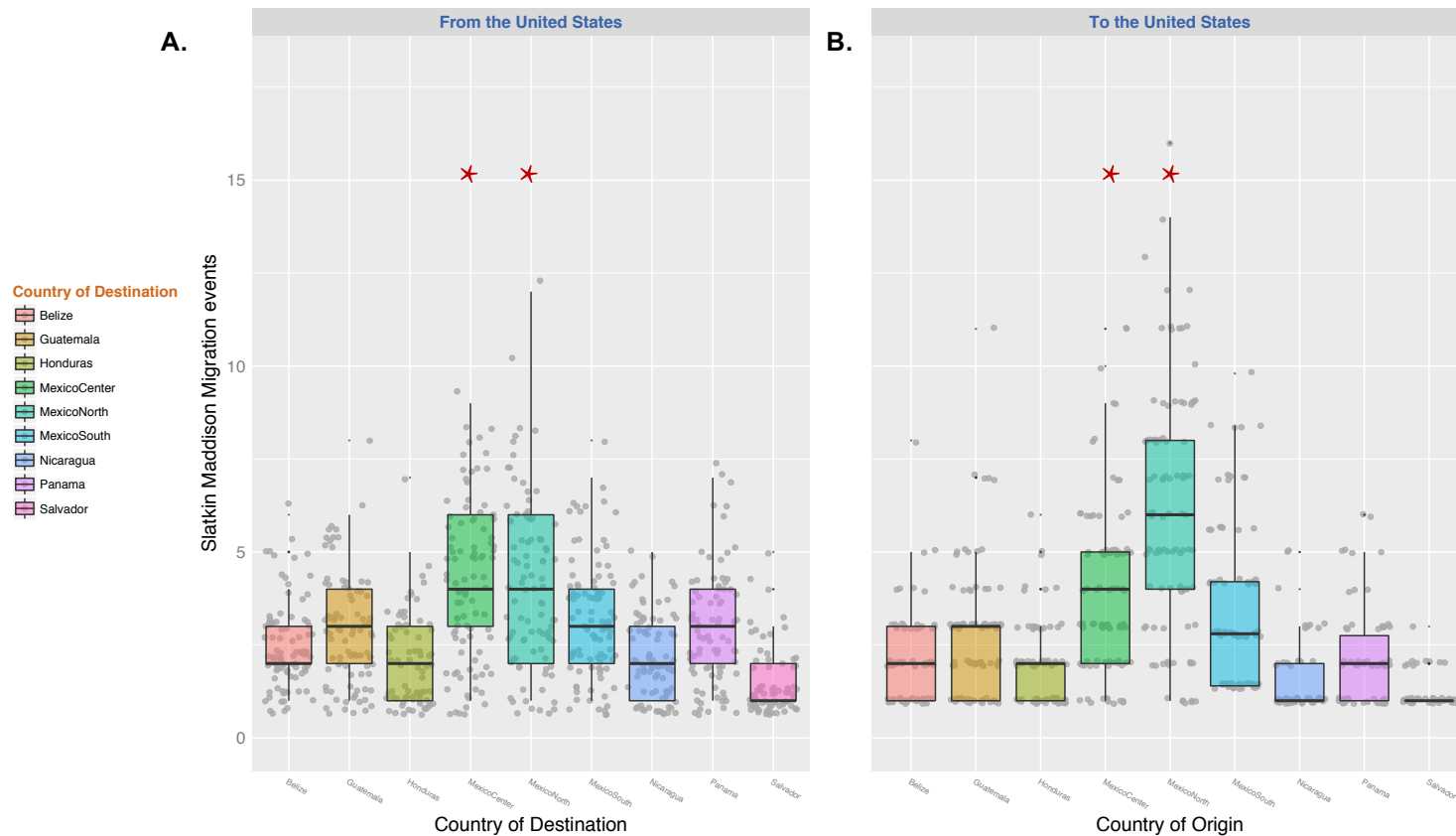
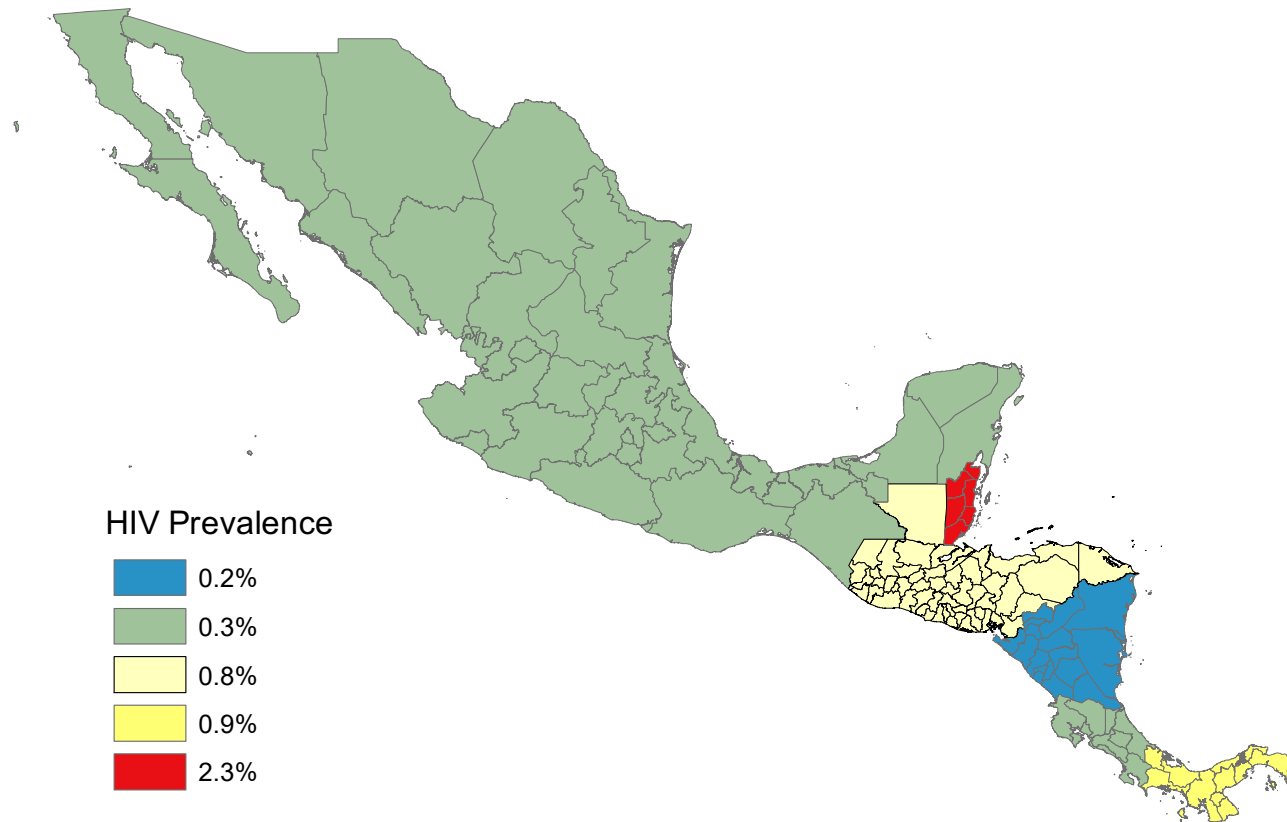


Figure S5. HIV Prevalence estimates in Central America and Mexico. Sources: USAID Report: HIV/AIDS profile for the Central American Region, February, 2011. UNGASS Report, Guatemala, 2010. TB, HIV/AIDS and other STs Programme Report, Belize, 2010. MSPAS, El Salvador, 2009. HIV/AIDS National Report, Honduras, June 2010. ECVC, Honduras, 2006. ECVC, Nicaragua, 2009. HIV/AIDS National Report, Costa Rica, 2009. Epidemiological Surveillance MINSA, MSPAS, Panama, 2010 (3) and in Mexico (4, 5).



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